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## SEQUENCE LISTING

<110> IMMUNEX CORPORATION  
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&lt;120&gt; ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR

&lt;130&gt; 3492-WO

<140> --to be assigned--  
 <141> 2004-11-04

<150> 60/518,166  
 <151> 2003-11-07

&lt;160&gt; 77

&lt;170&gt; PatentIn version 3.2

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 <213> Homo sapien

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ctg ctg cag gtg gca agc tct ggg aac atg aag gtc ttg cag gag ccc	96
Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro	
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acc tgc gtc tcc gac tac atg agc atc tct act tgc gag tgg aag atg	144
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met	
35                      40                       45	
aat ggt ccc acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg	192
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu	
50                      55                       60	
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Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly	
65                      70                       75                       80	
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Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala	
85                      90                       95	
gat aac tat aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag	336
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys	
100                    105                       110	

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tac agg gag ccc ttc gag cag cac ctc ctg ctg ggc gtc agc gtt tcc Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser 225 230 235 240	720
tgc att gtc atc ctc gcc gtc tgc ctg ttg tgc tat gtc agc atc acc Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr 245 250 255	768
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gag gag aat ggg ggc ttt tgc cag cag gac atg ggg gag tca tgc ctt Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu 420 425 430	1296
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Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met  
35 40 45

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu  
50 55 60

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly  
65 70 75 80

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala  
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Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys  
100 105 110

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn  
115 120 125

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser  
130 135 140

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala  
145 150 155 160

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn  
165 170 175

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys  
180 185 190

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr  
195 200 205

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser  
210 215 220

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser  
225 230 235 240

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr  
245 250 255

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser  
260 265 270

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu  
275 280 285

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn  
290 295 300

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg  
305 310 315 320

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser  
325 330 335

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp  
340 345 350

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro  
355 360 365

Val Glu Cys Glu Glu Glu Glu Val Glu Glu Lys Gly Ser Phe  
370 375 380

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu  
385 390 395 400

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly  
405 410 415

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu  
420 425 430

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe  
435 440 445

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro  
450 455 460

Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp  
465 470 475 480

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala  
485 490 495

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu  
500 505 510

Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro  
515 520 525

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln  
530 535 540

Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln  
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His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln  
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Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val  
580 585 590

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser  
595 600 605

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala  
610 615 620

Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly  
625 630 635 640

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly  
645 650 655

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser  
660 665 670

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp  
675 680 685

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val  
690 695 700

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu  
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Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr  
 725 730 735

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser  
 740 745 750

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly  
 755 760 765

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly  
 770 775 780

Ile Ser Glu Lys Ser Lys Ser Ser Ser Phe His Pro Ala Pro Gly  
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Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser  
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144  
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

atc ttt ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192  
 Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agg aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65                   70                   75                   80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85                   90                   95	
ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa	327
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
20                 25                   30	

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35                 40                   45	

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50                 55                   60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65                 70                   75                   80	

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc aac agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser	
20 25 30	

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

atc tat ggt gca tcc agc agg gcc cct ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	

cct gaa gat ttt gca gtg tat tac tgt cag cag tat gat cac tca gca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala	
85 90 95	

ggg tgg acg ttc ggc caa ggg acc aag gtg gag atc aaa	327
Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

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&lt;223&gt; Synthetic Construct

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser	
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Tyr Leu Ala Trp Tyr Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
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1                    5                    10                    15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag act gtt aac agc gac                    96  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Asn Ser Asp  
20                    25                    30

tac tta gcc tgg tac cag cag aaa ccg ggc cag gct ccc agg ctc ctc                    144  
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35                    40                    45

atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt                    192  
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50                    55                    60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag                    240  
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65                    70                    75                    80

cct gaa gat ttt gca gtc tat tac tgt cag cag tat ggt agg tca cct                    288  
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro  
85                    90                    95

ccg tgg acg ttc ggc caa ggg acc aaa gtg gat atc aaa                            327  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys  
100                    105

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&lt;223&gt; Synthetic Construct

&lt;400&gt; 8

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	20				25						30				

Tyr	Leu	Ala	Trp	Tyr	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35				40						45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50				55					60					

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65				70					75				80		

Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Arg	Ser	Pro
	85					90					95				

Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys
	100						105					

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&lt;212&gt; DNA

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&lt;220&gt;

&lt;223&gt; Light chain variable sequence

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&lt;221&gt; CDS

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&lt;400&gt; 9

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Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1			5						10					15		

gaa	aga	gcc	acc	ctc	tcc	tgc	agg	gcc	agt	cag	agt	gtt	agc	agc	gac	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asp	
	20				25							30				

tac	tta	gcc	tgg	tac	cag	cag	aaa	cct	ggc	cag	gct	ccc	agg	ctc	ctc	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	
	35				40						45					

atc tat ggt gca tct agc agg gcc tct ggc atc cca gac agg ttc agt Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser	192
50 55 60	
ggc agt ggg ttt ggg aca gac ttc act ctc acc atc agc aga ctg gag Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	240
65 70 75 80	
cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	288
85 90 95	
ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	327
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 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 11  
<211> 327  
<212> DNA  
<213> Artificial

&lt;220&gt;

&lt;223&gt; Light chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(327)

&lt;400&gt; 11

gat att gtg ctg acc cag tct cca gcc acc ctg tct ttg tct cca ggg	48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt aac agc aac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

atc tat ggt aca tcc tac agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

ggc agt ggg tct ggg aca gac ttc act ctc acc atc acc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu	
65 70 75 80	

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	

ccg tgg acg ttc ggc caa ggg aca cga ctg gag att aaa	327
Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys	
100 105	

&lt;210&gt; 12

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 12

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50                    55                    60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu  
 65                    70                    75                    80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85                    90                    95

Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
 100                    105

<210> 13

<211> 327

<212> DNA

<213> Artificial

<220>

<223> Light chain variable sequence

<220>

<221> CDS

<222> (1)...(327)

<400> 13

gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg	48
Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1                    5                    10                    15	

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser	
20                    25                    30	

tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu	
35                    40                    45	

atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50                    55                    60	

ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65                    70                    75                    80	

cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85                    90                    95	

ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa	327
Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100                    105	

<210> 14

<211> 109

<212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 14

Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 15  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 15  
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 16  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
115

<210> 17  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 17

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg	48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly	
1                       5                       10                       15	

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20                     25                       30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35                     40                       45	

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50                     55                       60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65                     70                       75                       80	

caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85                     90                       95	

aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr	
100                   105                       110	

gtc tcc tca	345
Val Ser Ser	
115	

<210> 18  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 18

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 19  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1) .. (345)

<400> 19  
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	
aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	
<210> 20	
<211> 115	
<212> PRT	
<213> Artificial	
<220>	
<223> Synthetic Construct	
<400> 20	
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	
Val Ser Ser	
115	

<210> 21  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 21		
gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg		48
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly		
1 5 10 15		
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat		96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn		
20 25 30		
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta		144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35 40 45		
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag		192
Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys		
50 55 60		
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt		240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu		
65 70 75 80		
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca		288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala		
85 90 95		
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc		336
Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr		
100 105 110		
gtc tcc tca		345
Val Ser Ser		
115		

<210> 22  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly		
1 5 10 15		

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 23

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 23

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
 Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 - 90 95

```

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
          100          105          110

```

gtc tcc tca  
Val Ser Ser  
115

<210> 24  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 24

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 25  
<211> 345  
<212> DNA  
<213> Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 25

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg	48
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

&lt;210&gt; 26

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 26

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 , 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 27  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1) .. (345)

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<400> 27
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg      48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1           5             10            15

```

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
           20              25                    30

```

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta      144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

```

```

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag      192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
      50          55          60

```

```

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65          70                  75                  80

```

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
                   85                 90                 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc      336  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100    105    110

gtc tcc tca      345  
 Val Ser Ser  
 115

<210> 28  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1    5    10    15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20    25    30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35    40    45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50    55    60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65    70    75    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85    90    95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100    105    110

Val Ser Ser  
 115

<210> 29  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220> 29  
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg  
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 . 15  
 48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 96

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 144

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc ttg aag  
 Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60  
 192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 240

caa atg aac agc ctg aga gcc gag gac atg gct ttg tat tac ttt gca  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 288

aga ggg agg tac tgg ttc ccg tgg ggc cag gga acc ctg gtc acc  
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 336

gtc tcc tca  
 Val Ser Ser  
 115  
 345

<210> 30  
 <211> 115  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 30

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15  
 1

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 2

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 3

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 31  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 31  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
1 . 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

gtc tcc tca  
Val Ser Ser  
115

345

<210> 32  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct  
<400> 32

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 33  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)...(345)

<400> 33  
gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336  
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

gtc tcc tca 345  
Val Ser Ser  
115

<210> 34  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                    70                    75                    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85                    90                    95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100                  105                  110

Val Ser Ser  
 115

<210> 35  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)...(345)

<400> 35  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg                    48  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1                        5                        10                        15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat                    96  
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20                      25                      30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta                    144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                      40                      45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag                    192  
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50                      55                      60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt                    240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65                      70                      75                      80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca                    288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85                      90                      95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc                    336  
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100                    105                    110

gtc tcc tca  
Val Ser Ser  
115

<210> 36  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 36

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1                   5                   10                   15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20                   25                   30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                   40                   45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50                   55                   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65                   70                   75                   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85                   90                   95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100               105               110

Val Ser Ser  
115

<210> 37  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)...(345)

<400> 37

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg  
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
1                   5                   10                   15

48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	96
20 25 30	
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
35 40 45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	192
50 55 60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	240
65 70 75 80	
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	288
85 90 95	
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	336
100 105 110	
gtc tcc tca Val Ser Ser 115	345

<210> 38  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct  
<400> 38

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
115

<210> 39  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 39  
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg  
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat  
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

```

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta      144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

```

```

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
      50          55          60

```

```

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65           70           75           .           80

```

```

caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
          85           90           95

```

```

aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

```

gta tcc tca 345  
Val Ser Ser  
115

<210> 40  
<211> 115

<212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 40

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 41  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)...(345)

<400> 41  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
35                                  40                                  45	
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	192
50                                  55                                  60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	240
65                                  70                                  75                                  80	
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr, Tyr Cys Ala	288
85                                  90                                  95	
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	336
100                                 105                                 110	
gtc tcc tca Val Ser Ser	345
115	

<210> 42  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct  
<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1                                 5                                 10                                 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20                                 25                                 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                                 40                                 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
50                                 55                                 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65                                 70                                 75                                 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85                                 90                                 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 43  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)...(345)

<400> 43  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30  
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60  
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80  
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336  
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110  
 gtc tcc tca 345  
 Val Ser Ser  
 115

<210> 44  
 <211> 115  
 <212> PRT  
 <213> Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 44

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1															
							5					10			15

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn
								20			25			30	

Ala	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
								35			40			45	

Ser	Gly	Ile	Gly	Thr	Gly	Gly	Ala	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
								50			55			60	

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
								65			70			80	

Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
								85			90			95	

Arg	Gly	Arg	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
								100			105			110	

Val	Ser	Ser
	115	

&lt;210&gt; 45

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 45

gag	gtt	cag	ttg	gtg	gag	tct	ggg	gga	ggc	ttg	gta	cag	cct	ggg	ggg
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1															48
								5			10			15	

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	aga	aat
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Asn
20															96
														30	

```

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta      144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

```

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

```

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65           70                      75          80

```

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

```

aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
          100          105          110

```

gtc tcc tca  
Val Ser Ser  
115

<210>	46
<211>	115
<212>	PRT
<213>	Artificial

<220>  
<223> Synthetic Construct

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
           50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
115

<210> 47  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1) .. (345)

<400> 47  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

```

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
          20           25           30

```

```

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta      144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

```

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192  
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

```

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65           70           75           80

```

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

```

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

```

gtc tcc tca  
Val Ser Ser  
115

<210> 48  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

&lt;400&gt; 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 49  
 <211> 345  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Heavy chain variable sequence

<220>  
 <221> CDS  
 <222> (1)..(345)

<400> 49  
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50                               55                               60	
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65                               70                               75                               80	
caa atg aac agc ctg aga gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85                               90                               95	
aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100                              105                               110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> 50  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly	
1                               5                                   10                               15	

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20                              25                               30	

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35                              40                               45	

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50                              55                               60	

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65                              70                               75                               80	

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85                              90                               95	

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr	
100                            105                               110	

Val Ser Ser  
115

<210> 51  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)...(345)

<400> 51		48
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg		
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly		
1                   5                   10                   15		
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat		96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn		
20                   25                   30		
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta		144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35                   40                   45		
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag		192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys		
50                   55                   60		
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt		240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu		
65                   70                   75                   80		
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca		288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
85                   90                   95		
aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc		336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr		
100                105                   110		
gtc tcc tca		345
Val Ser Ser		
115		

<210> 52  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 52

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly		
1                   5                   10                   15		

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

Val Ser Ser  
 115

<210> 53  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 53  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48  
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

```

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65           70           75           80

```

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
                   85              90              95

```

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc      336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
          100        105        110

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gtc tcc tca  
Val Ser Ser  
115

<210> 54  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
                   100                 105                 110

Val Ser Ser  
115

<210> 55  
<211> 345

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 55

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg  
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

96

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

144

tca ggt att ggt act ggt gcc aca agc tat gca gac tcc gtg aag  
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

240

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

288

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc  
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

336

gtc tcc tca  
 Val Ser Ser  
 115

345

&lt;210&gt; 56

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 56

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35                    40                    45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50                    55                    60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                    70                    75                    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85                    90                    95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100                  105                  110

Val Ser Ser  
 115

<210> 57  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1) .. (345)

<400> 57  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg                    48  
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1                    5                    10                    15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat                    96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20                  25                  30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta                    144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                  40                  45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag                    192  
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50                  55                  60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt                    240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65                  70                  75                  80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

```

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

```

gtc tcc tca  
Val Ser Ser  
115

<210> 58  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
           20                         25                         30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
           100                 105                 110

Val Ser Ser  
115

<210> 59  
<211> 345  
<212> DNA  
<213> Artificial

&lt;220&gt;

&lt;223&gt; Heavy chain variable sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(345)

&lt;400&gt; 59

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg  
 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

96

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta  
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

144

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag  
 Ser Gly Ile Gly Thr Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50 55 60

192

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt  
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65 70 75 80

240

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca  
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

288

aga ggg agg tac tgg tac ccg tgg ggc cag gga acc ctg gtc acc  
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100 105 110

336

gtc tcc tca  
 Val Ser Ser  
 115

345

&lt;210&gt; 60

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthetic Construct

&lt;400&gt; 60

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35                    40                    45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys  
 50                    55                    60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 65                    70                    75                    80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 85                    90                    95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
 100                    105                    110

Val Ser Ser  
 115

<210> 61  
<211> 345  
<212> DNA  
<213> Artificial

<220>  
<223> Heavy chain variable sequence

<220>  
<221> CDS  
<222> (1)..(345)

<400> 61  
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg         48  
Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1                    5                    10                    15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat         96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20                    25                    30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta         144  
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                    40                    45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag         192  
Ser Gly Ile Gly Thr Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50                    55                    60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt         240  
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65                    70                    75                    80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca         288  
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85                    90                    95

```

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc      336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
          100           105           110

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gtc tcc tca  
Val Ser Ser  
115

<210> 62  
<211> 115  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 62

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn  
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys  
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
65 70 75 80

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asp  
65 70 75

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ser  
115

<210> 63  
<211> 109  
<212> PRT  
<213> Artificial

<220>  
<223> 27A1 light chain variable region

<400> 63

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 64  
<211> 116  
<212> PRT  
<213> Artificial

<220>  
<223> 27A1 heavy chain variable region

<400> 64

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val  
35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser  
115

<210> 65  
<211> 107  
<212> PRT  
<213> Artificial

<220>  
<223> 5A1 light chain variable region

<400> 65

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
35 40 45

Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu  
85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 66  
<211> 123  
<212> PRT  
<213> Artificial

<220>  
<223> 5A1 heavy chain variable region

<400> 66

Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe  
20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys  
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu  
 65                   70                   75                   80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 67  
<211> 107  
<212> PRT  
<213> Artificial

<220>  
<223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp  
20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe  
 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105

<210> 68  
<211> 117  
<212> PRT  
<213> Artificial

<220>  
<223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ser Ile Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys  
85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser  
115

<210> 69  
<211> 107  
<212> PRT  
<213> Artificial

<220>  
<223> 1B7 light chain variable region

<400> 69

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ile Ala Ser Ile Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe  
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
 100 105

<210> 70

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primers

<220>

<221> misc\_feature

<222> (21)..(21)

<223> N is A or G

<220>

<221> misc\_feature

<222> (24)..(24)

<223> N is G or T

<400> 70

gtcgacgccc ccaccatgga nttnnnnnctg agctgg

36

<210> 71

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primers

<400> 71

cttgaccagg cagcccaagg c

21

<210> 72  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 72  
atcaaacgta cggcggctgc accatctgtc ttcattc

36

<210> 73  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 73  
gtttaaacgc ggccgcggat cctaacaactc tcccctgttg aagctcttt

49

<210> 74  
<211> 99  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 74  
gtcgacgccc ccaccatgga aaccccagcg cagcttctct tcctcctgct actctggctc

60

ccagataaccg ctagcgaaat tgtgttgacg cagtctcca

99

<210> 75  
<211> 99  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 75  
tggagactgc gtcaacacaa ttgcgttagc ggtatctggg agccagagta gcaggaggaa  
gagaagctgc gctgggttt ccatggtggc ggcgtcgac

60

99

<210> 76  
<211> 57  
<212> DNA  
<213> Artificial

<220>  
<223> Primers

<400> 76  
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<211> 327  
<212> PRT  
<213> Homo sapiens

<400> 77

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
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Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro  
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp  
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe  
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu  
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys  
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser  
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys  
325